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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/358,587

 DATE: 08/04/1999
 TIME: 12:40:30

Input Set: I358587.RAW

This Raw Listing contains the General Information
 Section and up to first 5 pages.

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1  <110> APPLICANT: Moore, et al.
2  <120> TITLE OF INVENTION: Keratinocyte Derived Interferon
3  <130> FILE REFERENCE: PF482
4  <140> CURRENT APPLICATION NUMBER: US/09/358,587
5  <141> CURRENT FILING DATE: 1999-07-21
6  <150> EARLIER APPLICATION NUMBER: 60/093,643
7  <151> EARLIER FILING DATE: 1998-07-21
8  <160> NUMBER OF SEQ ID NOS: 21
9  <170> SOFTWARE: PatentIn Ver. 2.0
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12 <212> TYPE: DNA
13 <213> ORGANISM: Homo sapiens
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19                                     Met Ser Thr Lys Pro Asp Met
20                                     1           5
21   att caa aag tgt ttg tgg ctt gag atc ctt atg ggt ata ttc att gct 103
22   ile gln lys cys leu trp leu glu ile leu met gly ile phe ile ala
23       10           15           20
24   ggc acc cta tcc ctg gac tgt aac tta ctg aac gtt cac ctg aga aga 151
25   gly thr leu ser leu asp cys asn leu leu asn val his leu arg arg
26       25           30           35
27   gtc acc tgg caa aat ctg aga cat ctg agt agt atg agc aat tca ttt 199
28   val thr trp gln asn leu arg his leu ser ser met ser asn ser phe
29       40           45           50           55
30   cct gta gaa tgt cta cga gaa aac ata gct ttt gag ttg ccc caa gag 247
31   pro val glu cys leu arg glu asn ile ala phe glu leu pro gln glu
32       60           65           70
33   ttt ctg caa tac acc caa cct atg aag agg gac atc aag aag gcc ttc 295
34   phe leu gln tyr thr gln pro met lys arg asp ile lys lys ala phe
35       75           80           85
36   tat gaa atg tcc cta cag gcc ttc aac atc ttc agc caa cac acc ttc 343
37   tyr glu met ser leu gln ala phe asn ile phe ser gln his thr phe
38       90           95          100
39   aaa tat tgg aaa gag aga cac ctc aaa caa atc caa ata gga ctt gat 391
40   lys tyr trp lys glu arg his leu lys gln ile gln ile gly leu asp
41      105          110          115
42   cag caa gca gag tac ctg aac caa tgc ttg gag gaa gac gag aat gaa 439
43   gln gln ala glu tyr leu asn gln cys leu glu glu asp glu asn glu
44      120          125          130          135

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45      aat gaa gac atg aaa gaa atg aaa gag aat gag atg aaa ccc tca gaa      487
46      Asn Glu Asp Met Lys Glu Met Lys Glu Asn Glu Met Lys Pro Ser Glu
47                      140                      145                      150
48      gcc agg gtc ccc cag ctg agc agc ctg gaa ctg agg aga tat ttc cac      535
49      Ala Arg Val Pro Gln Leu Ser Ser Leu Glu Leu Arg Arg Tyr Phe His
50                      155                      160                      165
51      agg ata gac aat ttc ctg aaa gaa aag aaa tac agt gac tgt gcc tgg      583
52      Arg Ile Asp Asn Phe Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp
53                      170                      175                      180
54      gag att gtc cga gtg gaa atc aga aga tgt ttg tat tac ttt tac aaa      631
55      Glu Ile Val Arg Val Glu Ile Arg Arg Cys Leu Tyr Tyr Phe Tyr Lys
56                      185                      190                      195
57      ttt aca gct cta ttc agg agg aaa taagaatcat ctaccttcaa gcaagaatta      685
58      Phe Thr Ala Leu Phe Arg Arg Lys
59      200                      205
60      acagagattg tggctacgca aatgcaccaa aaaaggggtga aatatatctg aaatgtacct      745
61      ggttctgccc ttggaagcca cttcctgctc atgccactaa cagcatgctg ccaaactgtt      805
62      cagattcaag attattccaa gcgcagggcc caaatgttat agccaaagaa agtcttatga      865
63      taaaagttag gcaaatttca gccagaagt tagaagagat gtttaaaaga acaagaacaa      925
64      attgtggatc atggtatatg caggctatca gcagaaggat cagacaataa aatgagttag      985
65      tgcaaaccat ttagtaaaaa taactatcag cagagttggt ccagattaaa aatagtacta      1045
66      caagcttgta aaggagttag gacatgcaag ctactgagca taaaatatat acttgctatt      1105
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76      Leu Met Gly Ile Phe Ile Ala Gly Thr Leu Ser Leu Asp Cys Asn Leu
77      20                      25                      30
78      Leu Asn Val His Leu Arg Arg Val Thr Trp Gln Asn Leu Arg His Leu
79      35                      40                      45
80      Ser Ser Met Ser Asn Ser Phe Pro Val Glu Cys Leu Arg Glu Asn Ile
81      50                      55                      60
82      Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr Gln Pro Met Lys
83      65                      70                      75                      80
84      Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu Gln Ala Phe Asn
85      85                      90                      95
86      Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu Arg His Leu Lys
87      100                     105                     110
88      Gln Ile Gln Ile Gly Leu Asp Gln Gln Ala Glu Tyr Leu Asn Gln Cys
89      115                     120                     125
90      Leu Glu Glu Asp Glu Asn Glu Asn Glu Asp Met Lys Glu Met Lys Glu
91      130                     135                     140
92      Asn Glu Met Lys Pro Ser Glu Ala Arg Val Pro Gln Leu Ser Ser Leu
93      145                     150                     155                     160
94      Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu Lys Glu Lys

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95          165          170          175
96      Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Ile Arg Arg
97          180          185          190
98      Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Phe Arg Arg Lys
99          195          200          205
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101 <211> LENGTH: 238
102 <212> TYPE: PRT
103 <213> ORGANISM: Homo sapiens
104 <400> SEQUENCE: 3
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107      Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
108          20          25          30
109      Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
110          35          40          45
111      Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
112          50          55          60
113      Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
114          65          70          75          80
115      His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
116          85          90          95
117      Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Glu Leu
118          100          105          110
119      His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
120          115          120          125
121      Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Val Pro Gln Leu Ser Ser
122          130          135          140
123      Leu Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu Lys Glu
124          145          150          155          160
125      Lys Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Ile Arg
126          165          170          175
127      Arg Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Pro Ala Leu Thr
128          180          185          190
129      Leu Arg Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys
130          195          200          205
131      Tyr Ser Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser
132          210          215          220
133      Leu Phe Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys
134          225          230          235
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138 <213> ORGANISM: Homo sapiens
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141          1          5          10          15
142      Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
143          20          25          30
144      Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg

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145           35           40           45
146 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
147           50           55           60
148 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
149           65           70           75           80
150 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
151           85           90           95
152 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
153           100          105          110
154 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
155           115          120          125
156 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
157           130          135          140
158 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
159           145          150          155          160
160 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
161           165          170          175
162 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
163           180          185
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165 <211> LENGTH: 194
166 <212> TYPE: PRT
167 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 5
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171 Gly Pro Phe Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu
172           20           25           30
173 Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser
174           35           40           45
175 Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu
176           50           55           60
177 Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu
178           65           70           75           80
179 His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser
180           85           90           95
181 Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu
182           100          105          110
183 His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly
184           115          120          125
185 Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Leu Ala Leu Lys Arg
186           130          135          140
187 Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp
188           145          150          155          160
189 Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser Ser
190           165          170          175
191 Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu Ser
192           180          185          190
193 Ser Pro
194 <210> SEQ ID NO 6

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197 <213> ORGANISM: Homo sapiens
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202           20           25           30
203   Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
204           35           40           45
205   Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
206           50           55           60
207   Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
208           65           70           75           80
209   His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
210           85           90           95
211   Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Glu Leu
212           100          105          110
213   His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
214           115          120          125
215   Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Val Pro Gln Leu Ser Ser
216           130          135          140
217   Leu Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu Lys Glu
218           145          150          155          160
219   Lys Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Ile Arg
220           165          170          175
221   Arg Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Pro Ala Leu Thr
222           180          185          190
223   Leu Arg Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys
224           195          200          205
225   Tyr Ser Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser
226           210          215          220
227   Leu Phe Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg
228           225          230          235          240
229   Asp Leu Gly Ser Ser
230           245
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233 <212> TYPE: PRT
234 <213> ORGANISM: Homo sapiens
235 <400> SEQUENCE: 7
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237       1           5           10           15
238   Lys Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
239           20           25           30
240   Gly Asn Arg Arg Ala Leu Ile Leu Leu Gly Gln Met Gly Arg Ile Ser
241           35           40           45
242   Pro Phe Ser Cys Leu Lys Asp Arg His Asp Phe Arg Ile Pro Gln Glu
243           50           55           60
244   Glu Phe Asp Gly Asn Gln Phe Gln Asp Ala Gln Ala Ile Ser Val Leu

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VERIFICATION SUMMARY
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PREVIOUSLY ERRORED SEQUENCES-EDITED

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3  <212> PRT
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9              20              25              30
10     Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
11             35             40             45
12     Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
13             50             55             60
14     Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
15             65             70             75             80
16     Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
17             85             90             95
18     His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
19             100            105            110
20     Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
21             115            120            125
22     Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
23             130            135            140
24     Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
25             145            150            155            160
26     Thr Gly Tyr Leu Gly Asn
27             165

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